

## Exhibit A

## Clean Version of The Pending Claims in U.S. Patent Application Ser. No. 09/975,308

- 1. (Amended) An isolated expression vector comprising the nucleotide sequence of SEQ ID NO:8.
- 2. (Amended) An isolated expression vector comprising a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:9.
  - 3. (New) A host cell comprising the recombinant expression vector of claim 1 or 2.

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## Exhibit B

## Marked Up Version of Amended Claims in U.S. Patent Application Ser. No. 09/975,308

- 1. (Amended) An isolated expression vector comprising the nucleotide sequence of SEQ ID NO:8.
- 2. (Amended) An isolated expression vector comprising a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:9.
  - 3. (New) A host cell comprising the recombinant expression vector of claim 1 or 2.

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ACCESSION:AB065623 NID: gi 21928520 dbj AB065623.1 Homo sapiens gene for seven transmembrane helix receptor, complete cds, isolate:CBRC7TM\_186
Length = 1324

Score = 617 bits (1575), Expect = e-175
Identities = 306/307 (99%), Positives = 307/307 (99%)
Frame = +3

Query: 1 MNHSVVTEFIILGLTKKPELQGIIFLFFLIVYLVAFLGNMLIIIAKIYSNTLHTPMYVFL 60
MNHSVVTEFIILGLTKKPELQGIIFLFFLIVYLVAFLGNMLIIIAKIY+NTLHTPMYVFL
Chick: 201 MNHSVVTEFIILGLTKKPELQGIIFLFFLIVYLVAFLGNMLIIIAKIY+NTLHTPMYVFL 380

Sbjct: 201 MNHSVVTEFIILGLTKKPELQGIIFLFFLIVYLVAFLGNMLIIIAKIYNNTLHTPMYVFL 380

Query: 61 LTLAVVDIICTTSIIPKMLGTMLTSENTISYAGCMSQLFLFTWSLGAEMVLFTTMAYDRY 120 LTLAVVDIICTTSIIPKMLGTMLTSENTISYAGCMSQLFLFTWSLGAEMVLFTTMAYDRY

Sbjct: 381 LTLAVVDIICTTSIIPKMLGTMLTSENTISYAGCMSQLFLFTWSLGAEMVLFTTMAYDRY 560

Query: 121 VAICFPLHYSTIMNHHMCVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPP 180

VAICFPLHYSTIMNHHMCVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPP Sbjct: 561 VAICFPLHYSTIMNHHMCVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPP 740

Ouery: 181 LLALSCSPVRINEVMVYVADITLAIGDFILTCISYGFIIVAILRIRTVEGKRKAFSTCSS 240

LLALSCSPVRINEVMVYVADITLAIGDFILTCISYGFIIVAILRIRTVEGKRKAFSTCSS

Sbjct: 741 LLALSCSPVRINEVMVYVADITLAIGDFILTCISYGFIIVAILRIRTVEGKRKAFSTCSS 920

Ouery: 241 HLTVVTLYYSPVIYTYIRPASSYTFERDKVVAALYTLVTPTLNPMVYSFQNREMQAGIRK 300

HLTVVTLYYSPVIYTYIRPASSYTFERDKVVAALYTLVTPTLNPMVYSFQNREMQAGIRK

Sbjct: 921 HLTVVTLYYSPVIYTYIRPASSYTFERDKVVAALYTLVTPTLNPMVYSFQNREMQAGIRK 1100

Query: 301 VFAFLKH 307

VFAFLKH

Sbjct: 1101VFAFLKH 1121

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